

SIC Sequence Search Report

SOURCE	Homo sapiens tissue_11b:placenta cDNA to mRNA..
ORGANISM	Homo sapiens

REFERENCE
1 (sites)
Ikegawa, S., Kumano, Y., Okui, K., Fujiwara, T., Takahashi, E. and
AUTHORS

TITLE	Isolation, characterization and chromosomal assignment of the human WNT7A gene cytogenet. Cell Genet. 74 (1-2), 149-152 (1996)
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MEDLINE 9/045094
REFERENCE 2 (bases 1 to 1442)
AUTHORS Nakamura, Y.
TITLE Direct Sublesion
JOURNAL Submitted (19-JAN-1996) to the DDBJ/EMBL/Genbank databases. Yuseke
 H. et al. (1996) Direct sublesion sequencing of DNA. *Methods Mol Biol* 106:1-12.

FEATURES

Location/Qualifiers

Nakamura, Institute Of Medical Science, The University Of Tokyo
Laboratory Of Molecular Medicine, 4-6-1 Shirokanedai, Minato-ku
Tokyo 108, Japan (E-mail: sikegawa@ims.u-tokyo.ac.jp,
Tel:+81-3-5440-5372, Fax:+81-3-5449-5433)

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CDS

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Db	91	CTCGGGAATCGGTGGCTTCTCTCAGTGTGACTGTGGCGCAAGCATCATCTGAACAAG	150
QY	121	atcccaagcgctggtctcccaagacagcggtcgatctgcagaagccggccgaagccatc	180
Db	151	ATCCCAAGCGGCTGCTCCAGACAGCGGGCATGTCCAGAGACCGGCCGACGCATCATC	210
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24	411	15.5	120	5	017149	NMT-A PROTEIN (FRAGMENT	2.68e-75
25	395	14.8	118	13	042116	NMT-4 (FRAGMENT).	4.29e-71
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27	364	13.7	128	5	076780	HYPOTHETICAL 14.4 KD P	5.20e-63
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29	337	13.4	118	5	017150	NMT-B PROTEIN (FRAGMENT	3.38e-61
30	345	13.0	111	5	096868	CELL SIGNALING MOLECUL	4.21e-58
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33	317	11.9	115	13	042118	NMT 6 (FRAGMENT).	6.08e-51
34	305	11.5	84	5	046281	WINGLESS (FRAGMENT).	6.63e-48
35	304	11.4	84	5	046281	WINGLESS (FRAGMENT).	1.19e-47
36	302	11.4	84	5	046301	WINGLESS (FRAGMENT).	3.79e-47
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ALIGNMENTS

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DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)			
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)			
DE	WNT1A PROTEIN.				
GN	WNT1A.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Euteria; Primates; Catarrhini; Hominoidea; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 97049094.				
RA	KIKEGAWA S., KUMANO Y., OKUI K., FUJIWARA T., TAKAHASHI E.,				
RA	NAKAMURA Y.;				
RT	"Isolation, characterization and chromosomal assignment of the human				
RT	WNT1A gene.";				
RL	Cytogenet. Cell Genet. 74:149-152(1996).				
CC	-1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING				
CC	MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF				
CC	TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY				
CC	SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE				
CC	EXTRACELLULAR MATRIX.				
CC	-1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.				
DR	EMBL: D83175; BAA82509.1; -				
DR	PROSITE: PS00246; WNT1.1.				
KM	Developmental protein; Glycoprotein.				
SO	SEQUENCE 349 AA; 39057 MW; 9C18E1B2 CRC32;				
	Query Match	99.4%;	Score 2643;	DB 4;	Length 349;
	Best Local Similarity 99.1%;	Pred. No. 0.0e+00;			
	Matches 346; Conservative 2;	Mismatches 1;	Indels 0;	Gaps	
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QY	1	MNRARCLGLHFLFSLGNYLRIGGFSSVALGASII CNKIPGLAPRQRAICGSRPDAI	60		
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2000, 03:22:17 ; Search time 528.89 seconds

(without alignments)
-6028.103 Million cell updates/sec

Title: US-09-459-774-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Search: 821193 seqs, -1518192014 residues

Total number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

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47: em_htg2: *
48: em_htg3: *
49: em_hum5: *
50: gb_p13: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	678.8	64.6	1449	12 MUSMNTVIB	M89802 Mouse Wnt-7
5	675.6	64.3	1948	4 PM080581	U80581 Pleurodeles
6	586	55.8	1199	4 AF026894	AF026894 Xenopus 1
7	482.2	45.9	245767	42 AC011607	AC011607 Homo sapi
8	479.6	45.7	1661	35 AF061975	AF061975 Branchios
9	297.4	28.3	1427	4 CHKW4P	D31900 Chicken mRN
10	292.6	27.9	1292	4 AF182403	AF182403 Gallus ga
11	289.4	27.6	1213	12 AF188608	AF188608 Rattus no
12	283	27.0	1101	12 MUSMNTIV	M89797 Mouse Wnt-4
13	283	27.0	1252	34 DMDWNT2MR	X64735 D.melanogas
14	283	27.0	1500	12 AF070988	AF070988 Mus muscu
15	276.8	26.4	3000	12 MUSINT4	M32502 Mouse proto
16	275	26.2	245767	42 AC011607	AC011607 Homo sapi
17	272.8	26.0	4114	9 HDMWNT5A	L20861 Homo sapien
18	261.2	24.9	2385	9 HSNWNT13	Z71621 H.sapiens W
19	254.6	24.2	2664	4 AMWNT5B	Z14048 A.mexicanum
20	252.2	24.0	369	4 PLEWNT7A	M91295 Plethodon j
21	248.8	23.7	1523	12 MUSMNTVB	M89799 Mouse Wnt-5
22	248.8	23.7	1690	12 MUSMNTVA	M89798 Mouse Wnt-5
23	248.8	23.7	1980	12 AF188333	AF188333 Rattus no
24	245.2	23.4	3056	35 AF061973	AF061973 Branchios
25	244	23.2	1509	4 DR051266	U51266 Danio rerio
26	243.2	23.2	369	4 GOOWNT7A	M91261 Chen caerul
27	241.6	23.0	369	4 TKYWNT7A	M91285 Meleagris g
28	241	23.0	1059	4 DR051414	U25141 Danio rerio
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31	235.6	22.4	2301	9 HSIHP	X07876 Human mRNA
32	235	22.4	1543	4 AB006014	AB006014 Gallus ga
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ALIGNMENTS

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DEFINITION Homo sapiens WNT7a mRNA, complete cds.
ACCESSION D83175
VERSION D83175.1 GI:5509900
KEYWORDS WNT7a.

PRI 16-JUL-1999

SOURCE Homo sapiens tissue_l1b:placenta cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Ikegawa,S., Kumano,Y., Okui,K., Fujiwara,T., Takahashi,E. and Nakamura,T.
TITLE Isolation, characterization and chromosomal assignment of the human WNT7A gene
JOURNAL Cytogenet. Cell Genet. 74 (1-2), 149-152 (1996)
MEDLINE 97049094
REFERENCE 2 (bases 1 to 1442)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1996) to the DDBJ/EMBL/GenBank databases. Yusuke Nakamura, Institute of Medical Science, The University of Tokyo, Laboratory of Molecular Medicine: 4-6-1 Shirokanebashi, Minato-ku, Tokyo 108, Japan (E-mail:ikegawa@ims.u-tokyo.ac.jp, Tel: +81-3-5449-5372, Fax: +81-3-5449-5433)
FEATURES
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Best Local Similarity 99.7%; Pred. No. 2.3e-188;
Matches 1047; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Oy 481 gcttcgccaaggtcttctgtgatgcccggagatcaagcaagatgcccgaactcatg 540
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Oy 541 aacttgcaacaacacggagcggcggcgaagatcctgtgaggaagaatgaagctggaatg 600
Db 571 AACTTGCAACAACGAGCGCGAGCGGCAAGATCTGTGAGGGAACATGAAGCTGGAAATGT 630
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Db 631 AAGTGCCAGCGCGTGTGAGGCTGCTGACACCAAGAGCTGTGGACCACTGCCCCAG 690
Oy 661 ttccggagcttggtgctacgtgtcacaagacaaagacaaagcgtgtcactgtgagcct 720
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HSU53476
LOCUS HSU53476 1469 bp mRNA PRI 19-MAY-1997
DEFINITION Human proto-oncogene Wnt7a mRNA, complete cds.
ACCESSION U53476
VERSION U53476.1 GI:2105099
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1469)
AUTHORS Bul,T.D., Iako,M., Lejeune,S., Curtis,A.R., Strachan,T., Lindsay,S. and Harris,A.L.
TITLE Isolation of a full-length human WNT7A gene implicated in limb development and cell transformation, and mapping to chromosome 3p25
JOURNAL Gene 189 (1), 25-29 (1997)
MEDLINE 97305141
REFERENCE 2 (bases 1 to 1469)
AUTHORS Bul,T.D., Lejeune,S. and Harris,A.L.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1996) T.D. Bul, Imperial Cancer Research Fund, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
FEATURES
Location/Qualifiers

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ORIGIN

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 DB 625 AAGTGCACAGCGGCTGTAGAGCTGTGACACCAAGACGAGCTGTGACACACTCCACAG 684
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 DB 865 GACCCGGTAGCCGCAAGTGTGGCACCAGCGCCGCTGTCAACAAGACGGCTCCCGAG 924
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 DB 925 GCCAGCGGCTGTGACCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 984
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 QY 961 gtgtgacagtgcaactgtaaatctccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
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 DB 985 GTGTGCAAGTCACTGTAAATCTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1044
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 QY 1021 gaggcagcagagatgtacagctgtgcaagtga 1050
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 DB 1045 GAGCGCAGGAGATGTACAGCTGCAAGTGA 1074

RESULT 3
 LOCUS MUSMNTVIIA 1050 bp mRNA
 DEFINITION Mouse Wnt-7a mRNA, complete cds.
 ACCESSION M89801
 VERSION M89801.1 GI:202409
 KEYWORDS Wnt-1 related protein; Wnt-7a protein; Int-1 related protein.
 SOURCE Mus musculus (strain C57/BL6) (library: lambda cDNA) 8.5 day embryo
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 REFERENCE 1 (bases 1 to 1050)
 Gavin,B.J., McMahon,J.A. and McMahon,A.P.
 Expression of multiple novel Wnt-1/Int-1-related genes during fetal
 and adult mouse development
 Genes Dev. 4, 2319-2332 (1990)
 JOURNAL MEDLINE 91122634
 REFERENCE 2 (sites)
 Gavin,B.J. and McMahon,A.P.
 Differential regulation of the Wnt gene family during pregnancy and
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 Mol. Cell. Biol. 12, 2418-2423 (1992)
 JOURNAL MEDLINE 92236617
 FEATURES
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 /organism="Mus musculus"
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 POFELVJLADKRIENVAHEPVRASNRNKLITKPLKSTRKMDJSDITILESPR
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BASE COUNT	234 a	296 c	324 g	196 t
ORIGIN				

Query Match	88.3%;	Score 926.8;	DB 12;	Length 1050;
Best Local Similarity	92.7%;	Pred. No. 5.4e-166;		
Matches 973;	Conservative 0;	Mismatches 77;	Indels 0;	Gaps 0;

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OY	61	ctccggaatcagctggctctctccctcagctgtacgtctctgtggcgcaacatcatctgtaaaga	120
Dp	61	CTCCGGAATCGGTTGGCTTCTCTCCGTTGGTACCTCTGGGTCCGAACATCATCTGTAAAG	120
OY	121	atcccaagcctgtgctctcccaagaacgagctctgtccagaagccgcccgaacgcatcatc	180
Dp	121	ATCCCAAGCCTGTGCTCCAGACACGGGGCAATCTCCAGAGCCGGCCGAGCCATCATC	180
OY	181	gtctatgaagaagaagctctcaaatgtggctgtgaacagatgtcaatgttcaatgttccgaatg	240
Dp	181	GTCTATGAGAAGAAGCTCTCCAAATATGGGCTTGACAGATGTAAGTTTCAGTTCCAAATAGG	240
OY	241	cgcctgaactctctctcagctgtgagagcgacacgctctctcggaagagagctcctaaagtgg	300
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Dp	361	GCTGCTGTCAACCCAGGCGAACCTTAGCGACTGTGGCTGCGCAAGAGGAAGCAAGGCGCAG	420
OY	421	taccacccggagcgaaggcgctgtgaagctgggtgtgctgtctctgcgaacatccgtaacgcatc	480
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Dp	481	GGCTTCGCGCAAGGCTCTTCTGTGAATGCCCGGAGATCAAGCAAGAAATGCCCGAGCTCATG	540
OY	541	aaacttgcacaaacaaacggagcgacgcgcgaagaagatctcttgaaagaaagaaatgcggaaatg	600
Dp	541	AACCTTACCAATAAACGAGCGCGGTGGAAAGTCTGTGAGGAGAAACATGAAGCTGTGAATGT	600
OY	601	aagtcgcaacgagcgtgtcacgctctgtgcaacaaagaacgctgtgaaacacactgtgccaa	660
Dp	601	AAGTGCATGTGTGTGTAAGCTCTCTGTAAACCAAGACGTGTGAGAACATCTGCCAAG	660
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Dp	661	TTCCGAGAGCTTAGGCTACGTCTCTCAAGAGCAAAATACAAGAGCGCCGTCCACGTGAGCCT	720
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Dp	781	CGCAAGCCCATGGAACCTGACACTGTGTATATCAAGTTGTCAACCCATTTACTGTGAAGAG	840
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Db	841	GACCCAGTACAGGCACAGCGTGGGTATACCCAGAGGCGCAGACCTTGCAATTAAAGACAGCCCTTACG	900
QY	901	gcccagcgcgcctctgacacccatcctatgctcgtctgtggcgtgtgtctacaacaccacccacgaagtcgcgcg	960
Db	901	GCCAGTGGCTCTGTACCTTCATGATGCTGTGGCGGTGGGTACACACACACACACAGTACGCCCGG	960
QY	961	gttggtggcagctgtcacactgttaagtctccaaatgtgtctgtctatgtcctaagtgacacacgtgtgcacg	1020
Db	961	GTGTGGCGAGTGCACCACTCCAAATTCCTCAATGTGGTGTCTCATCTCAAGTGTACACAGTGCACG	1020
QY	1021	gacgcgcacgagatctatcacacgtgcaagtga	1050
Db	1021	GAGCGCACGAGATGTATATACGTGCACAACTGA	1050

RESULT	4			
MUSMNTVIIIB				
LOCUS	MUSMNTVIIIB	1449 bp	mRNA	ROD
DEFINITION	Mouse Wnt-7b mRNA, complete cds.			27-APR-1993
ACCESSION	M89802			
VERSION	M89802.1	GI:202411		
KEYWORDS	Wnt-1 related protein; Wnt-7b; Int-1 related protein.			
SOURCE	Mus musculus (strain C57/BL6) (library: lambda cDNA)	8.5 day embryo		

REFERENCE	1 (bases 1 to 1449)
AUTHORS	Gavin, B.J., McMahon, J.A. and McMahon, A.P.
TITLE	Expression of multiple novel Wnt-1/Int-1-related genes during fetal and adult mouse development
JOURNAL	Genes Dev. 4, 2319-2332 (1990)
MEDLINE	91122634
REFERENCE	2 (sites)
AUTHORS	Gavin, B.J. and McMahon, A.P.
TITLE	Differential regulation of the Wnt gene family during pregnancy and lactation suggests a role in postnatal development of the mammary gland
JOURNAL	Mol. Cell. Biol. 12, 2418-2423 (1992)
MEDLINE	92336617
FEATURES	Location/Qualifiers

BASE COUNT	304 a	427 c	438 g	280 t
ORIGIN				

Query Match	64.6%	Score 678	8:	DB 12:	length 1449:
Best Local Similarity	77.9%	Pred. No. 3.5e-119:			
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					Gaps 0:
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Db	1	ATGCACAAAACTTTGGAAGCGAGTCTTTTACGCTGTTCTCTGCTTGGCGCTCCTAC	60		

LOCUS	PMU80581	1998 bp	DNA	VMT	02-JUN-1997
DEFINITION	Pleurodeles waltl Wnt-7a mRNA, complete cds.				
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Oy	241	gcgttgaaactctctgcacctggagagcgcaacgcttcttgggaaggggtcctcaagtggg	300		
Db	241	gccttgaaactctctgcacctggagagcgcaacgcttcttgggaaggggtcctcaagtggg	300		
Oy	301	agccggagagctgtgcttaccctaacatcatcttcgcccgcgctgtgcccagccatcaca	360		
Db	301	agtcagagagctgtgcttaccctaacatcatcttcgcccgcgctgtgcccagccatcaca	360		
Oy	361	gtctgctgtacccaagggcaacctgtgagcagctgtgctgtgcagaaagagaagcaaggccag	420		
Db	361	gctgctgtacccaagggcaacctgtgagcagctgtgctgtgcagaaagagaagcaaggccag	420		
Oy	421	taccacgggagcgaggtgtgaaatgggggtggtgctgctgtgcagatccgctcagcatc	480		
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Oy	481	ggtctgcgaaggtcttctgttgatgcccggagatctcaagcaaatgtccgagctctcatg	540		
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Oy	601	aagtgccacggcggtgtcaaggtctgtgtgacccaacgaagcgtgtgagccacaatctgcag	660		
Db	601	aagtgccacggcggtgtcaaggtctgtgtgacccaacgaagcgtgtgagccacaatctgcag	660		
Oy	661	tttcggaggtcgggtctacgtgtctcaagaagatacaagagcgctgtacgttggagacct	720		
Db	661	tttcggaggtcgggtctacgtgtctcaagaagatacaagagcgctgtacgttggagacct	720		
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Oy	781	cgcaagcccattgtagacagggacctgtgtatcatctgaagaatctgcgccaactctgcagag	840		
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Oy	901	gccagcggtctgtgacctatgtctgtctgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	960		
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ACCESSION U080581
 VERSION U080581.1 GI:2149106
 KEYWORDS
 SOURCE
 ORGANISM Iberian ribbed newt.
Pleurodeles waltl
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 Batrachia; Caudata; Salamandroidae; Salamandridae; Pleurodeles.
 REFERENCE 1 (bases 1 to 1948)
 AUTHORS Caudic,X., Nicolas,S. and Le Parco,Y.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-1996) LGPD, IBDM, CNRS-UNR C 9943, Parc
 Scientifique de Luminy, Marseille 13288, France
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 Best Local Similarity 78.4%; Pred. No. 1.4e-118;
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 QY 421 taacacgggagcagagctgtgaagtgggttggctgtcttcgcgacatccgctcaaggatc 480
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 QY 481 ggcttcggcaaggtctttgttgatgccccggagagtcaagcagaatgccggaactctatg 540
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Db	1273	GTGAGACCAAGCCGAAACAAGCGGCCAACCTCTCGAAGATCAAGAAACCTCTGTTTAC	1332
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Db	1393	GACCTGTCAACCGGTATGCGGGGTACACAGGGTAAATGTGCAACAAAGACGACACACAC	1452
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Db	1573	GAAGGACAGAGGTGTTTACTCTGTAGTGA	1602

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RESULT 6
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DEFINITION Xenopus laevis wnt7B (Xwnt7B) mRNA, complete cds.
ACCESSION AF026894
VERSION AF026894.1 GI:2583210
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae;
Xenopus.
1 (bases 1 to 1199)
Chang, C. and Hemmati-Brivanlou, A.
Neural patterning by Xenopus wnt7B gene
unpublished
2 (bases 1 to 1199)
Chang, C. and Hemmati-Brivanlou, A.
Direct Submision
Submitted (25-SEP-1997) Molecular Embryology, The Rockefeller
University, 1230 York Avenue, New York, NY 10021, USA
FEATURES
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BASE COUNT 325 a 277 c 326 g 271 t
ORIGIN

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OY	121	atcccaaggccgtgccccagacagcvggcgatcttgcgaagccggcccgcgcacatc	180
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Db	295	CGAATGGAATCTCTCGGGCGTGGGGGAAAAAGCGTCTTCGGTCAAGAGCTGCAAGTAGGA	354
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OY	361	gcctgcctttaccgaagggcnaacttgaacgtacttggctctgcgacaagaagaagcaagggcag	420
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Db	775	GTGAGAGCCAATTCCTTACGGGACACCCACCTTCTGTGAAGTACAAAAAAGTCCCAAGTTAC	834
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Db	835	CAGAAACCCATGAGAGAGGAGACTTGTGTACATTGAGAGGTCCTCCCAACTACTGTGAGGAG	894
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0y	955	actgatgctgtgaccttattgctcttgaggcctggtgctacattaccacagctatgacaaa								
0y	961	gtctgacagtcgaactcgttaagttccactggctgctgctatgtcaagtgcacacagctgacg								
Db	1015	gtttggcaatgcaactgtaagttccactggtctgtttttgaaatgcattactgacgt								
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DEFINITION										
SEQUENCING										
IN PROGRESS										
PIECES.										
PIECES.										
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GI:6087842										
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human.										
ORGANISM										
Homo sapiens										
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;										
Euthera, Primates; Catarrhini; Homidae; Homo.										
1 (bases 1 to 245767)										
Munzy,D.M., Adams,C., Bailey,M., Barbara,J., Blankenburg,K.,										
Bochler,B., Bouck,J., Bowle,S., Brooks,A., Bunay,C., Bunag,C.,										
Buckett,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C.,										
David,R., Delgado,O., Desharo,D., Ding,Y., Domah-Rashid,N.,										
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferriguto,D.,										
Forcum-Tansey,J., Frantz,P., Ganesh,R., Gorrrell,J.H., Gorrrell,L.L.,										
Guervar,M., Harris,K., Hernandez,J., Hodgson,A., Hoques,M.,										
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M.,										
Kelly,S., Kondolewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z.,										
Lichtarge,O., Liu,J., Liu,W., Logan,O., Lu,J., Lucier,R.,										
Martin,R., Martinez,C., McLeod,M.P., Mel,G., Morgan,M., Morris,S.,										
Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G.,										
Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Quiles,M.,										
Reiter,D., Rives,M., Samuel,S., Say,J., Scherer,S., Shah,E.,										
Shen,H., Simon,M., Sparks,A., Stamps,A., Sugeng,R., Tabor,P.,										
Taylor,T., Vasquez,L., Vinson,R., Vo,O., Wabhan,M., Wallington,S.,										
Weinstock,G., Weinstock,I.R., Williamson,A., Worley,K., Wren,J.,										
Wrenstord,G., Yu,W., Zhou,X., Nelson,D. and Gibbs,R.										
Direct Submission										
Unpublished										
2 (bases 1 to 245767)										
Worley,K.C.										
Direct Submission										
Submitted (08-OCT-1999) Human Genome Sequencing Center, Department										
of Molecular and Human Genetics, Baylor College of Medicine, One										
Baylor Plaza, Houston, TX 77030, USA										
On Oct 20, 1999 this sequence version replaced gi:6016014.										

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Db 1212 AA 1213

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LOCUS CHRM4P 1427 bp mRNA VR1 23-JUN-1999
DEFINITION Chicken mRNA for Wnt-4 protein, complete cds.
ACCESSION D31900
VERSION D31900.1 GI:505351
KEYWORDS Wnt gene family; Wnt-4 protein; cysteine-rich secretory protein; growth factor.
SOURCE Gallus gallus (library: lambda gt10) embryo cDNA to mRNA, clone Wnt-4.
ORGANISM Gallus gallus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (sites)
Yoshida, H., Ohuchi, H., Nohno, T., Fujiwara, A., Tanda, N., Kawakami, Y., and Noji, S.
Regional expression of the Cwnt-4 gene in developing chick central nervous system in relationship to the diencephalic neuromere D2 and a dorsal domain of the spinal cord
Biochem. Biophys. Res. Commun. 203 (3), 1581-1588 (1994)
2 (bases 1 to 1427)
Tanda, N., Kawakami, Y., Saito, T., Noji, S., and Nohno, T.
Cloning and characterization of Wnt-4 and Wnt-11 cDNAs from chick embryo
DNA Seq. 5 (5), 277-281 (1995)
3 (bases 1 to 1427)
Nohno, T.
Direct Submission
Submitted (20-JUN-1994) to the DDBJ/EMBL/GenBank databases. Tsutomu Nohno, Kawasaki Medical School, Department of Pharmacology; 577 Matsushima, Kurashiki, Okayama 701-01, Japan
(Tel:0864621111(ex.3637), Fax:0864621199)
Submitted (20-Jun-1994) to DDBJ by:
Tsutomu Nohno
Department of Pharmacology
Kawasaki Medical School
577 Matsushima
Kurashiki
Okayama 577
Japan
Phone: 0864-62-1111 x3637
Fax: 0864-62-1199.
FEATURES
SOURCE 1. 1427 Location/Qualifiers

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Best Local Similarity 59.7%; Pred. No. 3.7e-47;
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Lacher, M.D., Walthers, P.R., Lareu, R., Dharmarajan, A.M. and Frits, R.R.			2 (bases 1 to 1213)	2	2	2
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278	cacttgc	337				
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377	gcaacctgagc	436				
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437	gcttgag	496				
452	gttttcacgctgagc	511				

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QY	548	acaacaacagagagcgaagccggaagatccctctgagagagaaacatgaagcttgaaatgac	607
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Db	980	GCTGGCGCTGCGAGGTCCACATGCTGCTCTTGTCAAGTCCGCGACAGTGCAGCGGCTGC	1039
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VERSION	M89797.1 GI:202401		
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SOURCE	Mus musculus (strain C57/BL6) (library: Lambda cDNA) 8.5 day embryo cDNA to mRNA.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Gavin,B.J., McMahon,J.A. and McMahon,A.P.		
TITLE	Expression of multiple novel Mnt-1/Int-1-related genes during fetal and adult mouse development		
JOURNAL	Genes Dev. 4, 2319-2332 (1990)		
MEDLINE	91122634		
REFERENCE	2 (sites)		
AUTHORS	Gavin,B.J. and McMahon,A.P.		
TITLE	Differential regulation of the Mnt gene family during pregnancy and lactation suggests a role in postnatal development of the mammary gland		
JOURNAL	Mol. Cell. Biol. 12, 2418-2423 (1992)		
MEDLINE	92236617		
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Db	671	acggggtgctcgggctcctgcgaggtaaagacgtgctgcgctgtacccgccctccgcc	730
Qy	668	agcttggtctagctgtctcaagaaacaaagtccaaagagccgttcaactgtgaagctgtgctg	727
Db	731	aggttgccacagccgcttaagaggaagatttgacgggtgcacagaggtgagacacacacgcg	790
Qy	728	ccagccgcaacacagcgcacacactctctgaaagatcaagaagccactgctgtaacgcaagc	787
Db	791	taggtctctccggcgctgtgcttccgaaatgcaca-----gtttcaagccac	838
Qy	788	ccatgagacaggaactgtgtatcatcgyaaagtgcgcccaactactgcgaggaagcccg	847

Db	839	ATACAGATGAGGACCTGGTATACCTGGAGCCTAGCCCGGACTTCTGTGAGCAGGACATCC	898
Qy	848	tgaacggcagtgctggtgcaaccccaaggcgccgctgcaacaagacgctccccaagccaagcg	907
Db	899	GCAGTGGCGGTCTTAAAGCAGCAGAGGGGGCCGACAGTGCACAAAGACATCTTAAAGCCATTGACG	958
Qy	908	gctctgtaacctcaatgtgctgtgtggtgcgtgtgctaaacaccaccacgtaacgcccgtgtgtgc	967
Db	959	GCTGGGACCTCTCTGTGCTGTGGCCGCGCTTCACACAGGCAAGTGAAGACTGGCCAGGC	1018
Qy	968	agtgcaacttgaagtctcccaactggtctgcgtatgttgcacatgcacacgttgcagcgagcgca	1027
Db	1019	GCTGTGGCTGCAAGGTTCCACATGCTGCTCTCTTCGTCACAGTGCAGGCAAGTCCACAGGCGCTCG	1078
Qy	1028	cggagatgttacacgttgcacaagtga	1050
Db	1079	TGGAGATGCACACGTTGCCGGTGA	1101

RESULT	13
DMDWNT2MR	
LOCUS	DMDWNT2MR 1252 bp mRNA INV 09-AUG-1996
DEFINITION	D.melanogaster Dmwt-2 mRNA.
ACCESSION	X64735
VERSION	X64735.1 GI:7904
KEYWORDS	Dmwt-2 gene; wnt/wingless gene.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
AUTHORS	Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
TITLE	Drosophilidae; Drosophila.
	1 (bases 1 to 1252)
	Russell, J., Gemlissen, A. and Nusse, R.
	Isolation and expression of two novel wnt/wingless gene homologues
	in Drosophila
	Development 115 (2), 475-485 (1992)
JOURNAL	
MEDLINE	93048811
REFERENCE	2 (bases 1 to 1252)
AUTHORS	Nusse, R.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAR-1992) R. Nusse, Howard Hughes Medical Inst and
	Dept of Developmental Biology, Stanford University, Stanford CA
	94305, USA
FEATURES	
source	Location/Qualifiers
	1. 1252
	/organism="Drosophila melanogaster"
	/strain="Canton-S"
	/db_xref="taxon:7227"
	/dev_stage="embryo"
	/map="45E on polytene chromosome"
	29. 1087
	/gene="Wnt2"
	/note="Wnt oncogene analog 2"
	/allele=""
	/db_xref="FlyBase:FBgn004360"
	29. 1087
	/gene="Wnt2"
	/note="Dmwt-2"
	/codon_start=1
	/protein_id="CAA46001.1"
	/db_xref="GI:7905"
	/db_xref="FlyBase:FBgn004360"
	/db_xref="SWISS-PROT:P28465"
	/translation="MKINKKLITLYIMETRIYVSSFTSAMLCRIPELTGQRNMC
	REKPDALIAEGHQAGQCOHQFRGHSMSEVQNRVFNHVLPTASREAAIYAI
	ASGAAYRYTAACARGNISITCGDQVHRKATPTGGGTPDPMKGCSDAVDGRMAR
	RFMDARLEBDSRTLMNLNKRAGRTLVKMLRTDCKHGVSGSCVMKCKSLPER
	LVDDRLAMMYOKAKTVOAVKRGKGLVLSRKHGAGTAROKPVLDMPRMELIYEA
	SPRYCGRSLQTGSGTSGRTQRTGHPQSCDLLCCGRHNTHQIRRTTQCKRCQFMC
	CEVCKCECDSDIEFTCK"
CDS	
gene	
BASE COUNT	309 a 349 c 365 g 227 t 2 others
ORIGIN	

QY 827 actactcgcgagagagaccgcgtgaccgcagctgtggcaccaccagggccgcctgcaca 886
 Db 890 ACTTTGTGAGCCCAACCCAGAGAGGAGCTCTTGTGTACCGAGGACCGACTTGCAATG 949
 QY 887 agacgctcccccagggccagcgctgtgacctcaatgtctgtggcgctgtctacaacacc 946
 Db 950 TCACCTCCACGGGATGATGCTGCGATCTGTCTGTGCGCGGGCCCAACACGA 1009
 QY 947 accagtaagccgcgctgtgagtgcaactgttaagtccactgtgtgtctatgtcaagt 1006
 Db 1010 GGACGGAGAAACGGAGAGGAAATGCCATTGCGTCTTCACCTGCTGCTGTATGTACAGT 1069
 QY 1007 gcaacacgtgcagcgagcgacggagatgtacacgtgcagt 1048
 Db 1070 GCCAAGAGTGTATTCGATCTACGATGTGCACACCTGCAAGT 1111

rch completed: April 3, 2000, 04:12:53
 time: 3036 sec

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QY 121 AACTGNSIDCGDCEKQGYRDEGKMGWGGCSADIRYIGIKAFVADAREIKONARTLM 180
DB 181 NLHNEAGRKILIEENMKLECKCHGVSGSCTTKTCTTLPQFRELGYVLKDKINEAVHEP 240
QY 181 NLHNEAGRKILIEENMKLECKCHGVSGSCTTKTCTTLPQFRELGYVLKDKINEAVHEP 240
DB 241 VRASNNKRPFLIKIKKPLSYRRKPMDTLVYIEKSPNYCEEDPVTSVGTQGRACKNTAPQ 300
QY 241 VRASNNKRPFLIKIKKPLSYRRKPMDTLVYIEKSPNYCEEDPVTSVGTQGRACKNTAPQ 300
DB 301 ASGCDLMCCGGRGYNTHOYARVWCNCKFRHMCYKVCNCTCSETEMYTCK 349
QY 301 ASGCDLMCCGGRGYNTHOYARVWCNCKFRHMCYKVCNCTCSETEMYTCK 349

RESULT 2
ID 013266 PRELIMINARY: PRT: 348 AA.
AC 013266:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
WNT-7A.
Pleurodeles waltl (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Caudata; Salamandridae; Salamandridae; Pleurodeles.
RN [1]
RP SEQUENCE FROM N.A.
RA CAUBIT X., NICOLAS S., LE PARCO Y.;
RL Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL; U80581; AAB58494.1; -.
DR PROSITE; PS00246; WNT1.1.
DR Pfam; PF00110; wnt; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 348 AA: 39039 MW: 5951509 CRC32:

Query Match 89.7%; Score 2387; DB 13; Length 348;
Best Local Similarity 87.4%; Pred. No. 0.00e+00;
Matches 305; Conservative 30; Mismatches 13; Indels 1; Gaps 1;

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ID 042258 PRELIMINARY: PRT: 349 AA.
AC 042258:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
WNT7B.
GN XWNT7B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANG C., HEMMATI-BRIVANTLOU A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL; AF026894; AAB82725.1; -.
DR PROSITE; PS00246; WNT1.1.
DR Pfam; PF00110; wnt; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 349 AA: 39740 MW: 8665045 CRC32:

Query Match 83.2%; Score 2212; DB 13; Length 349;
Best Local Similarity 78.2%; Pred. No. 0.00e+00;
Matches 273; Conservative 50; Mismatches 26; Indels 0; Gaps 0;

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DB 1 MHRNRNMFVFLCFGIYKMLGALSSVALGANIICNKRIPGLAPROAICESRPDAI 60
QY 1 MHRNRNMFVFLCFGIYKMLGALSSVALGANIICNKRIPGLAPROAICESRPDAI 60
DB 61 IIEGAQMGINECOYQFRYGMWCSALGERTVFGQELRVSGREAAFTYATAGAAVAT 120
QY 61 IIEGAQMGINECOYQFRYGMWCSALGERTVFGQELRVSGREAAFTYATAGAAVAT 120
DB 121 SAGSGNSNCGDREKQGYNOEGKMGWGGCSADIRYIGISFAVADAREIKONARTLM 180
QY 121 SAGSGNSNCGDREKQGYNOEGKMGWGGCSADIRYIGISFAVADAREIKONARTLM 180
DB 181 NLHNEAGRKILIEENMKLECKCHGVSGSCTTKTCTTLPQFRELGYVLKDKINEAVHEP 240
QY 181 NLHNEAGRKILIEENMKLECKCHGVSGSCTTKTCTTLPQFRELGYVLKDKINEAVHEP 240
DB 241 VRASNNKRPFLIKIKKPLSYRRKPMDTLVYIEKSPNYCEEDPVTSVGTQGRACKNTAPQ 300
QY 241 VRASNNKRPFLIKIKKPLSYRRKPMDTLVYIEKSPNYCEEDPVTSVGTQGRACKNTAPQ 300
DB 301 TDGCDLMCCGGRGYNTHOYARVWCNCKFRHMCYKVCNCTCSETEMYTCK 349
QY 301 TDGCDLMCCGGRGYNTHOYARVWCNCKFRHMCYKVCNCTCSETEMYTCK 349

RESULT 4
ID 061700 PRELIMINARY: PRT: 347 AA.
AC 061700:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
WNT7B.
GN WNT7B.
OS Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
RN [1]
RP SEQUENCE FROM N.A.
RA SCHUBERT M., HOLLAND L.Z., JACOBS D.K., HOLLAND N.D.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING

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CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL: AF061975; AAC80433.1; -
DR PROSITE: PS00246; WNT1; 1.
DR PFAM: PF00110; wnt; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 347 AA; 39425 MW; CF2DA66 CRC32;

Query Match 69.3%; Score 1844; DB 5; Length 347;
Best Local Similarity 65.1%; Pred. No. 0.00e+00;
Matches 224; Conservative 69; Mismatches 46; Indels 5; Gaps 5;

Db 8 RYLGA-V-LCVA-1-LQGLSLTVVALGANIICNIPGLVPRRAICQTRPDLIVAGGA 64
7 RCLGLHFLSLGMVYLRIIGFSSVALGASIIICNIPGLAPRRAICQSRPAIIYIGSGS 66
65 QRGIDECVYQRRHSMNCTGDNNDVFRRLRIGSKFAFYTAISSALVHAIVTACSG 124
67 QMGDECFQFQRRHSMNCTGDNNDVFRRLRIGSKFAFYTAISSALVHAIVTACSG 126
125 NISDGGCDRTKEGDLN-DEGMMGCGSADVYKGLRCKKFPDAREVQNNARMLNHNNE 183
127 NLSDDGCDKEKQGYHRDEGMMGCGSADIRIGFAKVPDAREVQNNARMLNHNNE 186
184 AGRVVDQHTLECKCHGVSSTCTKTCITLTPREVENILKEKYHDAOLVENVARR 243
187 AGRILEENMMLLECKCHGVSSTCTKTCITLTPREVENILKEKYHDAOLVENVARR 245
244 TRPTFLKASRFEKREISLYLGRSPVNCERDEATGSLTGRRCNRTSPYQDCD 303
246 NKRPFLFKIKRPLSYKPMDDLYLIEKSPNCEPDPTGSGYQGRACNAPQASGCD 305
304 LMCGRGYNTHOYKTMQCNCKFHMCCYKNCQSEETETCK 347
306 LMCGRGYNTHOYKTMQCNCKFHMCCYKNCQSEETETCK 349

RESULT 5 PRELIMINARY; PRT: 385 AA.

ID 09YCX6;
AC 09YCX6;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
WNT-5A.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-EMBRYO;
RX MEDLINE: 99372672.
RA KAKAKAMI Y., WADA N., NISHIMATSU S., ISHIKAWA T., NOJI S., NOHNO T.;
RT "Involvement of Wnt-5a in chondrogenic pattern formation in the chick
RT limb bud."
RL Dev. Growth Differ. 41:29-40(1999).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL: AB060614; BAAT5242.1; -
DR PROSITE: PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 385 AA; 43005 MW; 1C8EA6D9 CRC32;

Query Match 41.2%; Score 1097; DB 13; Length 385;
Best Local Similarity 47.3%; Pred. No. 4.33e-265;

Matches 157; Conservative 67; Mismatches 90; Indels 18; Gaps 9;

Db 63 SEVYITGAOPLCSLAGISGCKKLYODHMOFIEGATGKECOYFRHRMNCST 122
27 SSVVALGASIIICNIPGLAPRRAICQSRPAIIYIGSGOMGDECFQFRRHSMNCSA 86
123 VDNNSVFRVMOQISREAFYTAISAGVAVMARRAGEEGSLGCGSRARPPDLPRD 181
87 LGERTVREKELVGSREAFYTAISAGVAVMARRAGEEGSLGCGSRARPPDLPRD 145
182 -WLMGCGSDNIETGYRFAKFEKVPDARERERYQKRSYSEARIMMLNHNNEAGRTVYNLAD 240
146 GMMKGGCSADIRIGFAKVPDARE--I--K---QARILMLNHNNEAGRTILEEMK 197
241 VACKCHGVSGSCLTKWLOADFRKVDALKEKYDSAANK-L-NSRCK---L-VQNN 293
198 LECKCHGVSGSCLTKWLOADFRKVDALKEKYDSAANK-L-NSRCK---L-VQNN 257
294 SRNAPRTIHDLYIDPSDYGMRNESGSLGTGRLCKTSEGMDGCELMKCGSGYDFK 353
258 LSYKPMDDTLYLIEKSPNCEPDPTGSGYQGRACNAPQASGCDLMCGRGYNTHQ 317
354 TVORERCHKRFHMCCYKCKLCTEIVDQFVCK 385
318 YARWQCNCKRFHMCCYKNCQSEETETCK 349

RESULT 6 PRELIMINARY; PRT: 331 AA.

ID 096867;
AC 096867;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE CELL SIGNALING MOLECULE WNT-5 (FRAGMENT).
GN SPWNT-5.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidae;
OC Echinozoa; Echinodermata; Echinozoa; Echinoidae; Strongylocentrotidae;
OC Strongylocentrotus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98320638.
RA FERKOWITZ M.J., STANDER M.C., RAFF R.A.;
RT "Phylogenetic relationships and developmental expression of three sea
RT urchin Wnt genes."
RL Mol. Biol. Evol. 15:809-819(1998).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL: U58982; AAC69436.1; -
DR PROSITE: PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein.
FT NON_TER
SQ SEQUENCE 331 AA; 36989 MW; A94F2700 CRC32;

Query Match 40.8%; Score 1086; DB 5; Length 331;
Best Local Similarity 50.2%; Pred. No. 5.69e-262;
Matches 164; Conservative 53; Mismatches 92; Indels 18; Gaps 10;

Db 14 LGTGPLSELGSLSPGOOLCOLYODHMAPIGGAKSIDSCQNOFTRRNCSVDSSNN 73
32 LGASTICKIKIGLAPRRAICQSRPAIIYIGSGOMGDECFQFRRHSMNCALGERT 91
74 VFGVYLSSRREAFYTAISAGVAVMARRAGEEGSLGCGSRARPPDLPRD--VWVG 131
92 VFGKELVGSREAFYTAISAGVAVMARRAGEEGSLGCGSRARPPDLPRD--VWVG 150
132 GCGSNIDYGFARFAPDAREMETNPGQSFAYRBMKMLNHNNEAGRTVYNLADGCTCK 191

Oy	151	GCSADIRYIGIGPAKVFVDAREIKQA-R---T---L-MNLHNNAAGRIILENNKLBCKC	202
Dd	192	HGVSSGSLCTKWCLQLSPFNRYGTILKKKYGCATNV--RV--NKGR-L-VNSDARPNK	244
Oy	203	HGVSSGCTTKCMTLLPQFRELGYVLKMKYNEAVHEVPVARSRRKPFLFKRPFSYRK	262
Dd	245	PTRDLVYLQSPDYCLDIOTGSLSGTGRNCNNTSMGDSCTLMCCGGRYNSTKEVE	304
Oy	263	PMDDLVYEIESPNYCDEDPVTGSVGTOGRACNKTAPQASCDMLMCCGGRYNHQIARW	322
Dd	305	RCKRKFMCVCYVKCRKCRTLVDVHYCK	331
Oy	323	QCNCRFHWCYVKCNTCSERTENTYCK	349
RESULT	7	PRELIMINARY;	PRT; 361 AA.
ID	O9YSC0		
AC	O9YSC0:		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
PT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
PR	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
WT	WN16 PROTEIN.		
OS	WN16.		
OC	Homo sapiens (Human).		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PLACENTA;		
RA	BARNES M.R., KELSEID D.P., FEAR M.W.;		
RT	"Cloning and characterization of human Wnt16, a novel member of the		
RL	Wnt gene family."		
DR	Submitted (May-1999) to the EMBL/GenBank/DBJ databases.		
SQ	EMBL; AF152584; AAD38052.1; "		
	SEQUENCE 361 AA; 40558 MW; D59A8ED6 CRC32;		
Query Match	39.1%; Score 1040; DB 4; Length 361;		
Best Local Similarity	44.6%; Pred. NO. 6,02e-249;		
Matches 145; Conservative	76; Mismatches 85; Indels 19; Gaps 11.		
Dd	43	CANLP-LMSROKELCKRRPYLLPSIREGARLGIOECRSOFERHMNCMTAATTAPGA	101
Oy	38	CNKIGGLPPOBAIQSPDAIIYIGESSQGLDECQGFENGRMNC-----SA-LGE	89
Dd	102	SPLEFEELSGETKETAFIYVAAGAIVSVYRSCSAGNMTCSDTTLLONGSASEGMHW	161
Oy	90	RTVEFEEKLVGSRREAAFIYAIIAGVAHAITAACTOGLSDCGGDKEKGQGHHDGKMV	149
Dd	162	GGCSDVDVOYGMEFSKKELDFFIGNTGKENVLLAMNIHNNEAGROAVAKIMSYDCRCHG	221
	150	GGCSMDIRYIGFAFVFD-AR-EIK-ONARTL--MNHNNEAQRKIIEENMKLECKCHG	204
Dd	222	VSGCAVATCKMKTSSFEKIGHLKDKXENSIQSD-KIKRKMRR-EKDORKIPIHK--	277
Oy	205	VSGSTTYTCWTTLPQFRELGYVLKDKYNEAVHEVPVARSRRKPFLKIKPLSYRPM	264
Dd	278	D-DLLYVKSPPNYCYEDKKLIGPGQRECARSTSEGADCMILCCGGRYNTHVHVARERC	336
Oy	265	DTDLYVIEKSNYCEDEPVTVSGVIGQACAKKTAPOASGCDLMCCGGRYNHTQIARWOC	324
Dd	337	ECKFTWCYVRCCRCEKTDVHTCK	361
Oy	325	NCKFHMCCYVKCNCTCSERTENTYCK	349
RESULT	8	PRELIMINARY;	PRT; 370 AA.
ID	P79752		
AC	P79752:		
DT	01-MAY-1997 (TREMBLrel. 03, Created)		
PT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)		
PR	01-NOV-1999 (TREMBLrel. 12, Last annotation update)		
WT	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OS	WN1.		

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
CC	Tetraodonfliformes; Tetraodontidae; Tetraodontoideae; Echinoidea.
NC	(1)
RN	SEQUENCE FROM N.A.
RP	GELTNER K., BRENNER S.:
RA	Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RL	-I- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY).
CC	-I- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX.
CC	-I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR	EMBL; AF061116; AAC34388.1; -
DR	PROSITE; PS00246; WNT1; 1.
DR	Pfam; PF00110; wnt; 1.
KM	Developmental protein; Glycoprotein.
SQ	SEQUENCE 370 AA; 41050 MW; 1412B124 CRC32:
	Query Match 38.0%; Score 1010; DB 13; Length 370; Best Local Similarity 43.5%; Pred.No.1.82e-240; Matches 135; Conservative 67; Mismatches 100; Indels 8; Gaps 6;
Df	LSRRRRIIRONPGILHAIAGLIAAIGLAIAKEKCWCORNRNRMCPPTTHSAVYGGKYNGRCRE 122 :: :: :: :: Oy 44 LAPROATCOGRPAIIIVIEGSSOMGDCECFOPFORNMCRMSALGERTVGKKLKVSRE 103 ::
Df	TAFFVAIASGVATHAVASCSGEAIEPCTCQRYRGEP--GGPDWHMGGSNDVNEFGMFIS 180 ::
Oy	AALTAYITAAAGVANAHTACTOGNLSDCGCDCKEKQGYYHHDEGNKGCCSADIRYGIFA 163 ::
Df	REFVDSSRGHDRLYLTLHNENEGMYTSSEMRBECKCHGMSSCATVTQRMKRLPSFRM 240 ::
Oy	KVFVDAREIKQNARTIAMLNHNENAGRILEBNMKTLECKHGYSVCSTTCMCMTLLPFGRE 223 ::
Df	VGFDFLKDPEFDSAKRVYAANKSGNSASHAPRHLPENP-AHKPPSMGLVIYEKSFNFC 239 ::
Oy	LGYVLKDKDYKNNAVHE-PVRAS-R-NKR--PTFLKIKPKPLSYRKPMDDLDLVYEKSPNYC 278 ::
Df	SYSGTGTLGHSGRANCNSTSPDGCCELLOGBRFKRTISMTERHCCTPHNCHVSCLN 359 ::
Oy	BBDPYTGSGVGIOGRCAKNTAFQAOSGCDLMCCGRGYNTHQYRWQCNCCKTFHMCCCYAKCNT 338 ::
Df	CSTRRTLHQ C 369 ::
Oy	CSEIREMYTC 348 ::
RESULT 9	PRELIMINARY; PRT; 252 AA.
ID AC	P91951 PRELIMINARY; PRT; 252 AA. P91951.
Dt	01-MAY-1997 (TREMBLE1_03, Created) 01-MAY-1997 (TREMBLE1_03, Last sequence update) DT 01-NOV-1999 (TREMBLE1_12, Last annotation update) Dt WNT-4 PROTEIN (FRAGMENT). DE GN HEMWT-4. OS Hellocarditis erythrogramma (Sea urohin). OC Eukaryote; Metazoa; Echinodermata; Echinozoa; Echinoidea; NC Euechinoidea; Echinoacea; Echinoida; Echinosmetridae; Hellocarditis. RN (1) RP SEQUENCE FROM N.A. RA FERROWICK M.J.; STANDER M.C.; RAFF R.A.; RL J.Mol.Evol. 0:0-0(0) Cc -I- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALLING MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY SIMILARITY). Cc -I- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE EXTRACELLULAR MATRIX. Cc -I- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY. DR EMBL; U88626; AAC69242.1; -. DR PROSITE; PS00246; WNT1; 1.

244 SNNKPTFLIKKIPSLYKRPMDTDLVIYIKSPNYCEDPVTSGTQGFACNKTAPQASG 303
Db 309 CGLMCCGGRYNAATYELVERCOCKYHMCYSCCTCKRTVERYVSK 354
Oy 304 COLMCCGGRYNTHOYARVWQCNCKFHMCCYVNCNCTSETEMYTCK 349

RESULT 12
ID 09WUD6; PRELIMINARY; PRT; 350 AA.
AC 09WUD6;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE WNT8B PROTEIN PRECURSOR.
GN WNT8B.
OS Mus musculus (Mouse).
OC Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RC RICHARDSON M., REDMOND D., WATSON C., MASON J.O.;
RT "Mouse Wnt8b is expressed in the developing forebrain and maps to
chromosome 19.";
RL Mamm. Genome 0:0-0(1999).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX.
CC CC
CC EMBL; AF130349; AAD31816.1; -.
DR PROSITE; PS00246; WNT1; 1.
KM Developmental protein: glycoprotein.
SQ SEQUENCE 350 AA; 38576 MM; 89442A96 CRC32;

Query Match 32.9%; Score 875; DB 11; Length 350;
Best Local Similarity 42.4%; Pred. No. 1,85e-202;
Matches 125; Conservative 64; Mismatches 94; Indels 12; Gaps 8;

Db 42 VAAGASGIEECKYOPAMRNMCPERALDLSHG-GLRSANETAVVAHAISSAGWYITL 100
Oy 62 IEQSOMGLDECOFQFRNRNMCALG-ERTYFGEKELKYSREAPATYAIAGVAHAIT 120
Db 101 RNCSLGDFNCGCDDSRNGOLG-GGCMWLGSGSDNYGFEAISKOPVDALETGODARAM 159
Oy 121 AACTGNTLSDCCGDKKQGYHDEBGMKGGCSADIRYIGIRAKYFVDAREIKONARTLM 180
Db 160 NLHNEAGRAVAKGTMKRTCKHGVSGSCTQTQWLDPEFREYVAHLKRYAHLKVDL 219
Oy 181 NLHNEAGRAKILLENMKLECKHGVSGSCTTCTQWLTQFRELGYVLADKYNENAVHVR 240
Db 220 LOGAGNSAAGRAIAD--TFRSISTRELVHLEDSPLYCKENTLGLLGTGEGRECLRRGA 277
Oy 241 VASARKRPTFLKIKKPLSRKPMPTDLYIIEKSPNYCEDPVTSGVSGRAC--NKT 297
Db 278 LGRWERSRCRLCGDGLAVEERRAETVSSCKCFHMCACVCEOCRRVTVYFC 332
Oy 298 -AP-QASGCDLMC--CGRGYNTHOYARVWQCNCKFHMCCYVNCNCTSETEMYTTC 348

RESULT 13
ID 023224; PRELIMINARY; PRT; 398 AA.
AC 023224;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE W0802.1 PROTEIN.
GN W0802.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderidae; Caenorhabditis.

[1]
RN SEQUENCE FROM N.A.
RP SWINBURNE J., AINSCOUGH R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIR M., JOHNSTON L.,
RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SPALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN K., VAUGHAN K., WATERSTON R.,
RA WATSON A., WAINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 270271; CAA94237.1; -.
DR PFMW; PF00110; wnt; 1.
SQ SEQUENCE 398 AA; 45843 MM; F54ACC1 CRC32;

Query Match 30.9%; Score 822; DB 5; Length 398;
Best Local Similarity 39.8%; Pred. No. 1.28e-187;
Matches 135; Conservative 79; Mismatches 96; Indels 29; Gaps 19;

Db 63 ICRRLDGLNPNOALCAENPSPFVARGVREARECECKRKFERNWSSDDEVETPHG 122
Oy 37 ICNKIPGLAPORALCOSRPAITVIGESQMGDECOFQFRNGWNSA--LGE-R-- 90
Db 123 KFODILGTLRSANKEAFNAIMASIVHITKGCNTGTEGCDG-SKPMQRYQAES 181
Oy 91 T--VFGELEKYGSRFAFTYAIAGVAHAITACITGNSDCCGDKERKQ-Q-YHND- 144
Db 182 DPMNRDQFSWGGCSDNYPHGIRAKKFLDWEAQAQFDKTNVAHLVRHNNFYGREAIA 241
Oy 145 E--G-W-K--MGCSADIRYIGIRAKYFVDAREIKQ-N-ARTLMN--HNNEAGRAKILE 193
Db 242 QNIRQCRCHGVSGCEKRTQWLMQKSOVSDDLKKRYHFNAYVELEDYTR-KATRL 300
Oy 194 ENMKLECKCHGVSGSCTTCTQWLTLPQRELGYVLADKYN--AVHVEVRASRNKRPTFL 252
Db 301 R-RKERTERKIPLRNGENAAVYHRSPLYCEKNIYLGILTSRECIHNSSESDLLCCG 359
Oy 253 KIKKRLSYRK-PM-DTDLVIYIEKSPNYCEDPVTSGVSGRACNKTAPQASGCDLMCCG 310
Db 360 RGYNTREIROTQCECKFVWCCEYKCKTCEBAVHTCK 398
Oy 311 RGYNTHOYARVWQCNCKFHMCCYVNCNCTSETEMYTCK 349

RESULT 14
ID P79753; PRELIMINARY; PRT; 390 AA.
AC P79753;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE WNT10B.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN [1]
RP SEQUENCE FROM N.A.
RP GELINER K., BRENNER S.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE

EXTRACELLULAR MATRIX.

CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

DR EMBL: AF056116; AAC34389.1; -

DR PROSITE: PS00246; WNT1.1.

DR PIRAM: PF00110; wnt.1.

KW Developmental protein; Glycoprotein.

SQ SEQUENCE 390 AA; 43656 MW; B432800B CRC32;

Query Match 29.8%; Score 793; DB 13; Length 390;

Best Local Similarity 40.3%; Pred. No. 1,59e-179; Mismatches 100; Indels 33; Gaps 19;

Matches 141; Conservative 76; Mismatches 100; Indels 33; Gaps 19;

Db 42 LTPNSVCLKLAGSKRQMRKCVSPDAPASALQIOVAIHCOYQLRDQRMNCSLEGLG 101

Y 32 LGASIIKIKIGLAPQALQSRDPAITIVGESQMGIDLCQFQFRGNCSL-G-E 89

Db 102 KLPHNNTLNGFRSASFLMLAAGVAHVASACSMGKLKGGCEAKRRODDKIRKL 161

Y 90 R-TVFGKELKVGSRPAFTYAIAGVAHAITACTGCLDCCGD-K-----EK----- 137

Db 162 TOLQLOSLKNDLSMOETWEGSDHVRVGRDRSRLMDLRSRSPRDIHAKMKIHNRV 221

Y 138 -Q-G-Q-YHRE--G---WKGCCSADIRYIGPAKVFVDREIKQARTLMLHNEA 187

Db 222 GQIYTDNMRKCKCHGTSGSCQFQTCWVSPERLVGSLKEKELSAIIVNSQKNNGV 281

Y 188 GKILEEMMKLECKCHGVSCTTKTTLQFRELGYLKDKNENAVHEP-VRAS-R 245

Db 282 FNPRIGSVSGSTGLNGRRSRSLVYFEKSPFCEPMLSDVDSAGTGRICKTSQS 341

Y 246 -NKR-PTFLKIKRP-LS--YRKPMOTDLYIEKSPNYCEEDPVTSVGTGRACKRTAPQ 300

Db 342 TDSGSLCCGGRHNLTKHSEKCRFHMCCYVCECRL-TEWYVCK 390

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Db 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Y 301 ASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

Search completed: Thu Mar 30 12:44:05 2000
Job time : 94 secs.

Y 92 -V-FGKEL-KVGSREAFYTAIIAGVAHAITACTGCLDCCGD-KEKQG--Y----- 141

Db 159 HRLOLEMMNRKGVHGVLEHMPSEVPGPOETWEGGSPDVEGERSPKDFLAREMYR 218

Y 142 HR-----D---E---G---WKGCCSADIRYIGPAKVFVDREIKQARTLMLHNEA 174

Db 219 DIHARMLHNNRQVAVLDNMGKCKCHGTSGSCQFQTCWVSPERLVGSLKEKELSAIIVNSQKNNGV 278

Y 175 NARTLMLHNNRQVAVLDNMGKCKCHGTSGSCQFQTCWVSPERLVGSLKEKELSAIIVNSQKNNGV 234

Db 279 ATLIRP-H-NRNTQOV-DHGIIPIRRRSSINS-LVFEKSPFCESEPPOLDSDAGTGRIC 334

Y 235 AVHVEPYVASRNRKPTFLKIKRPLSYRKPMOTDLYIEKSPNYCEEDPVTSVGTGRACKRTAPQ 294

Db 335 NKTSPGDNCSLCCGGRHNLTKHSEKCRFHMCCYVCECRL-TEWYVCK 389

Y 295 NKTAPQASGCDLMCGGNTHOYARWQCNCKFHMCCYVCAKNTCSERTE-MYTK 349

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